



## COMPLETE MICROBIOME MAPPING

### General Macroscopic Description

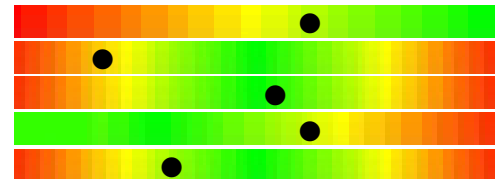
	Result	Markers
Stool Colour	<b>Brown</b>	<b>Colour</b> - Brown is the colour of normal stool. Other colours may indicate abnormal gut health.
Stool Form	<b>Semiformed</b>	<b>Form</b> -Sample form is categorised using the Bristol stool chart. A comment on stool appearance can be found in the comments section.
Mucous	<b>Not Detected</b>	<b>Mucous</b> - Mucous production may indicate the presence of an infection and/or inflammation.
Occult Blood	<b>POSITIVE</b>	<b>Blood (Macro)</b> - The presence of blood in the stool may be the result of several causes besides colorectal bleeding, including hemorrhoids or gastrointestinal infection.

### Short Chain Fatty Acids

Result Range Units

Methodology: GC/MS

Short Chain Fatty Acids, Beneficial	16.1	> 13.6	umol/g
Butyrate	11.1	10.8 - 33.5	%
Acetate	63.2	44.5 - 72.4	%
Propionate	23.4	0.0 - 32.0	%
Valerate	2.3	0.5 - 7.0	%

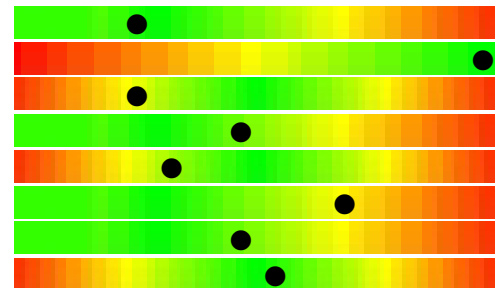


### GIT Functional Markers

Result Range Units

Methodology: FEIA, EIA, CLIA, pH electrode

Calprotectin.	8.6	0.0 - 50.0	ug/g
Pancreatic Elastase	>800.0	> 200.0	ug/g
Secretory (slgA)	700.5	510.0 - 2040.0	ng/mL
Zonulin	47.6	0.0 - 107.0	ng/mL
Beta glucuronidase	1928.7	368.0 - 6266.0	U/g
Steatocrit	9.0	0.0 - 10.0	%
a-Transglutaminase IgA	56.0	0.0 - 100.0	units/L
pH	7.2	6.3 - 7.7	



### Microbiome Mapping Summary

#### Parasites & Worms

#### Bacteria & Viruses

#### Mycology

#### Key Phyla Microbiota

##### Firmicutes:Bacteroidetes Ratio

0.12 < 1.00

RATIO



Relative Commensal Abundance of the 6 Phyla groups can be found on page 6 of this report



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-.SHIREE WALKER  
GLOW AESTHETICS PERTH  
54B ANGOVE STREET  
NORTH PERTH WA 6006

**KRYSTIELEE HARRISON**  
**10-Sep-1987**      **Female**

11 FREEMAN VIEW  
BUSHMEAD WA 6055

LAB ID : 4115353  
UR NO. : 6662742  
Collection Date : 23-Jun-2025  
Received Date: 25-Jun-2025



4115353

## Parasites and Worms.

### Parasitic Organisms

Result	Range	Units	
<dl	< 1.0	x10 <sup>5</sup> org/g	●
<dl	< 1.0	x10 <sup>5</sup> org/g	●
<dl	< 1.0	x10 <sup>5</sup> org/g	●
<dl	< 1.0	x10 <sup>5</sup> org/g	●
<dl	< 1.0	x10 <sup>5</sup> org/g	●
<dl	< 1.0	x10 <sup>5</sup> org/g	●
<dl	< 5.0	x10 <sup>5</sup> org/g	●
<dl	< 1.0	x10 <sup>5</sup> org/g	●

### Worms

<b>Ancylostoma duodenale, Roundworm</b>	<b>Not Detected</b>		
<b>Ascaris lumbricoides, Roundworm</b>	<b>Not Detected</b>	<b>Necator americanus, Hookworm</b>	<b>Not Detected</b>
<b>Trichuris trichiura, Whipworm</b>	<b>Not Detected</b>	<b>Enterobius vermicularis, Pinworm</b>	<b>Not Detected</b>
<b>Enterocytozoon spp</b>	<b>Not Detected</b>	<b>Hymenolepis spp, Tapeworm</b>	<b>Not Detected</b>
<b>Strongyloides spp, Roundworm</b>	<b>Not Detected</b>	<b>Taenia species, Tapeworm</b>	<b>Not Detected</b>

Comment: Not Detected results indicate the absence of detectable DNA in the sample for the worms reported.

NOTE: Reflex testing is performed on clinically indicated samples

## Opportunistic Bacteria/Overgrowth

Result	Range	Units	
<dl	< 1.00	x10 <sup>4</sup> CFU/g	●
<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
<dl	< 1.00	x10 <sup>4</sup> CFU/g	●
<dl	< 3.00	x10 <sup>4</sup> CFU/g	●
0.16	< 1.00	x10 <sup>3</sup> CFU/g	●
<dl	< 5.00	x10 <sup>3</sup> CFU/g	●
<dl	< 3.00	x10 <sup>4</sup> CFU/g	●
0.25	< 1.00	x10 <sup>6</sup> CFU/g	●
<dl	< 1.00	x10 <sup>4</sup> CFU/g	●
<dl	< 1.00	x10 <sup>6</sup> CFU/g	●
<dl	< 5.00	x10 <sup>6</sup> CFU/g	●
<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
<dl	< 18.00	x10 <sup>6</sup> CFU/g	●
<dl	< 5.00	x10 <sup>5</sup> CFU/g	●

### Potential Autoimmune Triggers

<dl	< 5.00	x10 <sup>4</sup> CFU/g	●
4.08	< 5.00	x10 <sup>4</sup> CFU/g	●
<dl	< 5.00	x10 <sup>3</sup> CFU/g	●
<dl	< 5.00	x10 <sup>5</sup> CFU/g	●
<dl	< 1.00	x10 <sup>9</sup> CFU/g	●
<dl	< 5.00	x10 <sup>5</sup> CFU/g	●
<dl	< 1.00	x10 <sup>4</sup> CFU/g	●
3.96	< 20.00	x10 <sup>4</sup> CFU/g	●



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Mycology	Result	Range	Units	
Candida dubliniensis.	<dl	< 1.00	x10^5 CFU/g	
Candida glabrata.	<dl	< 1.00	x10^5 CFU/g	
Candida intermedia.	<dl	< 1.00	x10^5 CFU/g	
Candida krusei.	<dl	< 1.00	x10^5 CFU/g	
Candida lambica.	<dl	< 1.00	x10^5 CFU/g	
Candida lusitaniae.	<dl	< 1.00	x10^5 CFU/g	
Candida parapsilosis.	<dl	< 1.00	x10^5 CFU/g	
Candida tropicalis.	<dl	< 1.00	x10^5 CFU/g	
Candida albicans.	<dl	< 1.00	x10^5 CFU/g	
Candida famata.	<dl	< 1.00	x10^5 CFU/g	
Candida keyfr.	<dl	< 1.00	x10^5 CFU/g	
Candida lipolytica.	<dl	< 1.00	x10^5 CFU/g	
Geotrichum species.	<dl	< 1.00	x10^5 CFU/g	
Rhodotorula species.	<dl	< 1.00	x10^5 CFU/g	
Saccharomyces cerevisiae:	<dl	< 1.00	x10^5 CFU/g	



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Bacterial Pathogens:	Result	Range	Units	
Aeromonas hydrophila.	<dl	< 1.00	x10 <sup>3</sup> CFU/g	
Campylobacter species.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	
C. difficile, Toxin A	<dl	< 1.00	x10 <sup>4</sup> CFU/g	
C. difficile, Toxin B	<dl	< 1.00	x10 <sup>4</sup> CFU/g	
Enteraggregative E. coli	<dl	< 1.00	x10 <sup>3</sup> CFU/g	
Enteropathogenic E. coli	<dl	< 1.00	x10 <sup>3</sup> CFU/g	
E. coli O157	<dl	< 1.00	x10 <sup>2</sup> CFU/g	
Hypervirulent Clostridium difficile	<dl	< 1.00	x10 <sup>3</sup> CFU/g	
Enteroinvasive E. coli/Shigella	<dl	< 1.00	x10 <sup>3</sup> CFU/g	
Enterotoxigenic E. coli LT/ST	<dl	< 1.00	x10 <sup>5</sup> CFU/g	
Salmonella species.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	
Shiga toxigenic E.coli	<dl	< 1.00	x10 <sup>3</sup> CFU/g	
Vibrio species.	<dl	< 1.00	x10 <sup>4</sup> CFU/g	
Yersinia species.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	
Helicobacter pylori	<dl	< 1.0	x10 <sup>3</sup> CFU/g	

Comment: Helico Pylori virulence factors will be listed below if detected **POSITIVE**

Gene: A2142C	Not Detected		
Gene: A2142G	Not Detected		
Gene: A2143G	Not Detected		
H.pylori Virulence Factor, babA	Not Detected	H.pylori Virulence Factor, cagA	Not Detected
H.pylori Virulence Factor, oipA	Not Detected	H.pylori Virulence Factor, vacA	Not Detected
H.pylori Virulence Factor, virB	Not Detected	H.pylori Virulence Factor, virD	Not Detected

Viral Pathogens	Result	Range	Units
Adenovirus 40/41	Not Detected		
Norovirus GI/II	Not Detected		
Rotavirus A	Not Detected		
Sapovirus (I,II,IV,V)	Not Detected		
Astrovirus (hAstro)	Not Detected		



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Normal Bacterial GUT Flora.	Result	Range	Units	
<i>Bacteroides fragilis</i>	290.0*H	1.6 - 250.0	x10 <sup>5</sup> CFU/g	
<b>TOTAL BIFIDOBACTERIA</b>	<b>38.4</b>	5.0 - 2000.0	x10 <sup>6</sup> CFU/g	
<i>Bifidobacterium adolescentis</i>	<dl	4.6 - 1000.0	x10 <sup>6</sup> CFU/g	
<i>Bifidobacterium bifidum</i> .	<dl	4.6 - 1000.0	x10 <sup>6</sup> CFU/g	
<i>Bifidobacterium breve</i> .	<dl	4.6 - 1000.0	x10 <sup>6</sup> CFU/g	
<i>Bifidobacterium longum</i>	38.4	4.6 - 1000.0	x10 <sup>6</sup> CFU/g	
<i>Enterococcus species</i>	458.3	1.9 - 2000.0	x10 <sup>3</sup> CFU/g	
<i>Escherichia species</i>	4046.2*H	3.7 - 3800.0	x10 <sup>4</sup> CFU/g	
<b>TOTAL LACTOBACILLI</b>	<b>1.6*L</b>	1.7 - 3000.0	x10 <sup>3</sup> CFU/g	
<i>Lactobacillus acidophilus</i> .	<dl	1.7 - 500.0	x10 <sup>3</sup> CFU/g	
<i>Lactobacillus casei</i> .	<dl	1.7 - 500.0	x10 <sup>3</sup> CFU/g	
<i>Lactobacillus delbrueckii</i>	1.5*L	1.7 - 500.0	x10 <sup>3</sup> CFU/g	
<i>Lactobacillus plantarum</i> .	<dl	1.7 - 500.0	x10 <sup>3</sup> CFU/g	
<i>Lactobacillus rhamnosus</i>	0.2*L	1.7 - 500.0	x10 <sup>3</sup> CFU/g	
<i>Lactobacillus salivarius</i>	<dl	1.7 - 500.0	x10 <sup>3</sup> CFU/g	
<i>Clostridium species</i>	15.3	5.0 - 50.0	x10 <sup>7</sup> CFU/g	
<i>Oxalobacter formigenes</i>	<dl *L	> 5.00	x10 <sup>6</sup> CFU/g	
<i>Akkermansia muciniphila</i>	8.31	1.00 - 50.00	x10 <sup>7</sup> CFU/g	
<i>Faecalibacterium prausnitzii</i>	220.0	100.0 - 3500.0	x10 <sup>6</sup> CFU/g	

A total count of *Lactobacillus* and *Bifidobacterium* has been included to offer a broad overview of the species present in the microbiome, which may assist in guiding clinical treatment decisions. However, identifying individual strains of *Lactobacillus* and *Bifidobacterium* can yield more detailed and clinically specific information, as different strains exhibit distinct physiological effects, as outlined in the probiotics action chart below.

## Actions







	<i>S. thermophilus</i> FP4	<i>S. boulardii</i> CNCM I-1079	<i>B. longum</i> Rosell-75	<i>L. rhamnosus</i> Rosell-11	<i>L. helveticus</i> Rosell-52	<i>L. salivarius</i> LS03	<i>L. fermentum</i> LF10	<i>B. breve</i> B632	<i>L. salivarius</i> LS01	<i>L. fermentum</i> LF16	<i>B. longum</i> 04	<i>L. rhamnosus</i> LR06	<i>L. plantarum</i> LP01	<i>B. animalis</i> subsp. <i>lactis</i> BA05	<i>L. crispatus</i> strains	<i>L. fermentum</i> LF08	<i>B. breve</i> BR03	<i>L. casei</i> LC03	<i>B. animalis</i> subsp. <i>lactis</i> BS01	<i>L. acidophilus</i> LA02	<i>L. rhamnosus</i> GG	<i>L. plantarum</i> 299V	<i>L. plantarum</i> 6595	<i>L. plantarum</i> HEAL19	<i>L. paracasei</i> 8700:2	<i>L. plantarum</i> HEAL9
Intestinal epithelial barrier health																										
Mucous membrane health																										
Normalisation of bowel movements																										
Normalisation of bloating																										
Normalisation of peristalsis																										
Autoimmune immunomodulation																										
Inhibition of pathogenic overgrowth																										
Inactivate microbial toxins																										
Increase infection resistance																										
Th1/Th2 immune cell modulation																										
Staphylococci inhibition																										
Gut-brain axis support																										
GABA production																										
Bone resorption inhibition																										
E. coli inhibition																										
Oxalate degradation																										



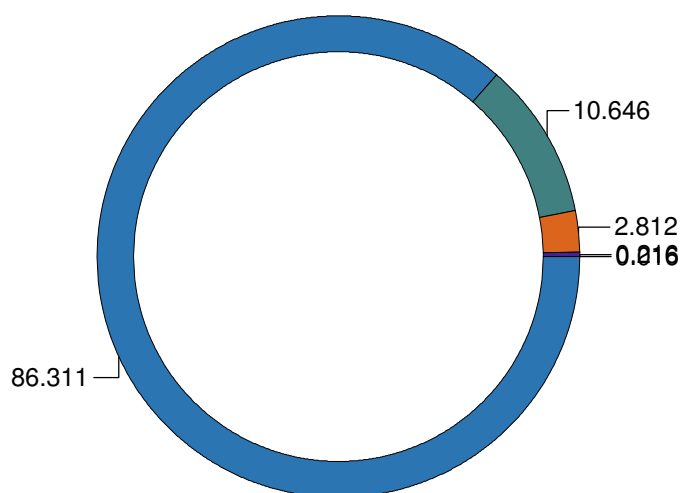
4115353

#### Introduction:

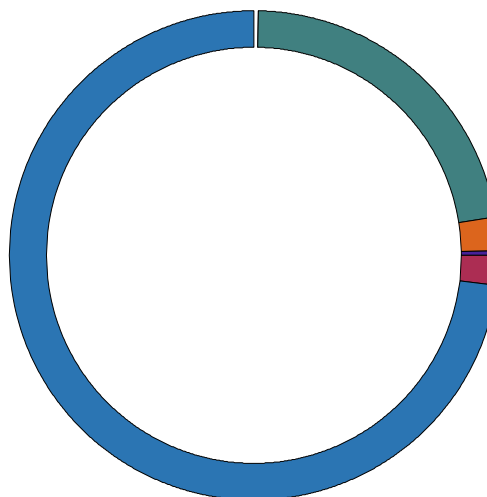
Your gut microbiome is a collective name for the 40 trillion cells and up to 1000 microbial species that include bacteria, viruses, fungi, parasites, and archaea and reside in our gut. The number of gut bacterial cells is approximately equal to the total number of human cells in our body, so if we consider only cell counts, we are only about half human. In terms of gene counts, the microbiome contains about 200 times more genes than the human genome, making bacterial genes responsible for over 99% of our body's gene content! Of all the microbial communities in the human body, the gut microbiome is by far the most dense, diverse, and physiologically important ecosystem to our overall health.

Relative Commensal Abundance	Result	Range	Units
 Bacteroidetes Phylum	86.311	50.000 - 95.000	%
 Firmicutes Phylum	10.646	3.500 - 40.000	%
 Proteobacteria Phylum	2.812	0.050 - 12.500	%
 Verrucomicrobia Phylum	0.216	0.000 - 2.400	%
 Actinobacteria Phylum	0.016	0.001 - 4.818	%
 Euryarchaeota Phylum	0.000	0.000 - 0.010	%

**Your Phyla:**



**Healthy Phyla:**



#### References:

NOTE: Relative abundance reference ranges have been based on a healthy population study.

King CH, et., al. (2019) Baseline human gut microbiota profile in healthy people and standard reporting template. PLoS One. 2019 Sep 11;14(9):e0206484.



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## Pathogen Summary:

### Macroscopy Comment

BROWN coloured stool is considered normal in appearance.

A SEMI-FORMED stool specimen classified as Type 4 on the Bristol Stool Chart is generally considered optimal, indicating balanced gut motility, adequate hydration, and sufficient dietary fibre intake. This stool consistency is often associated with efficient digestion, proper colonic function, and microbial stability. However, while Type 4 stools typically suggest gastrointestinal homeostasis, they do not always correlate with a healthy gut microbiome. Pathogenic bacteria, viral infections, parasitic infestations, or gut dysbiosis may still be present, even in well-formed stools. Clinical recommendations include maintaining a fiber-rich diet with prebiotic and probiotic sources, ensuring consistent hydration, and promoting gut microbial diversity through fermented foods or supplementation.

### FAECAL OCCULT BLOOD POSITIVE:

Faecal occult blood has been detected in this specimen. The presence of blood in the stool may be the result of several causes besides colorectal bleeding, including hemorrhoids or gastrointestinal infection. Results should be considered with other clinical information available to the physician.

Please note: A positive result indicates that the sample likely contains a human haemoglobin concentration >20ng/ml (Limit of detection).

Review this result with other inflammation markers such as calprotectin.

### Metabolism Comment

In a healthy gut Short Chain Fatty Acids (SCFAs) exhibited in the following proportions; Butyrate, Acetate, Propionate (16%:60%:24%).

The primary SCFAs butyrate, propionate and acetate are produced by predominant commensal bacteria via fermentation of soluble dietary fibre and intestinal mucus glycans.

Key producers of SCFAs include *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Bacteroides fragilis*, *Bifidobacterium*, *Clostridium* and *Lactobacillus* Spp.

The SCFAs provide energy for intestinal cells and regulate the actions of specialised mucosal cells that produce anti-inflammatory and antimicrobial factors, mucins that constitute the mucus barriers, and gut active peptides that facilitate appetite regulation and euglycemia. Abnormal SCFAs may be associated with dysbiosis, intestinal barrier dysfunction and inflammatory conditions.





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## **GIT Markers Comment**

**PANCREATIC ELASTASE:** Normal exocrine pancreatic function.

Pancreatic Elastase reflects trypsin, chymotrypsin, amylase and lipase activity.

This test is not affected by supplements of pancreatic enzymes.

Healthy individuals should be producing >500 ug/g of PE-1 under normal/healthy conditions.

PE-1 levels between 200 - 500 ug/g may indicate suboptimal production.

PE-1 levels <200 ug/g indicate clear inadequate production.

The clinician should therefore consider digestive enzyme supplementation if one or more of the following conditions is present:

Loose watery stools, Undigested food in the stools, Post-prandial abdominal pain, Nausea or colicky abdominal pain,

Gastroesophageal reflux symptoms, Bloating or food intolerance.

Testing performed by chemiluminescence immunoassay (CLIA).

**CALPROTECTIN Normal:**

Faecal calprotectin values <50 ug/g are not indicative of inflammation in the gastrointestinal tract. Subjects with low faecal calprotectin levels normally do not need to be further investigated by invasive procedures. In patients with strong clinical indications of intestinal inflammation, repeat testing may be useful.

Test performed by Diasorin Liaison XL chemiluminescent immunoassay (CLIA).

**SECRETORY IGA NORMAL:**

Secretory IgA is within range.

Secretory IgA represents the first line of defence of the gastrointestinal mucosa and is central to the normal function of the gastrointestinal tract as an immune barrier. Review this level with other pathogenic bacteria and normal commensal flora. Lower levels within reference range should be interpreted clinically.

**ZONULIN NORMAL:**

Zonulin is a protein that modulates intestinal barrier function. This results is considered normal.

**Beta-GLUCURONIDASE NORMAL:**

B-Glucuronidase is considered normal and is within reference range.





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## Normal Bacterial Flora Comment

**BACTEROIDES FRAGILIS ELEVATED:**

PHYLUM: Bacteroidetes

### DESCRIPTION:

*Bacteroides fragilis* is an anaerobic, Gram-negative bacterium. It is part of the normal microbiota of the human colon and is generally commensal. *Bacteroides fragilis* plays an intricate role in the human colon and usually has a beneficial relationship with the host. However, elevated levels may be potentially pathogenic. Disruption of tissue barriers and the spread of *Bacteroides fragilis* into adjacent tissue can cause polymicrobial infection. Enterotoxigenic *Bacteroides fragilis* (ETBF) strains are strains of *B. fragilis* that secrete an enterotoxin termed the *B. fragilis* toxin (BFT) and may have a role in inflammatory diarrhea and flare-ups of inflammatory bowel disease.

**TREATMENT SUGGESTIONS:** If treatment is warranted, Piperacillin/tazobactam, meropenem, and metronidazole have high susceptibility rates.

**BIFIDOBACTERIUM ADOLESCENTIS LOW:**

PHYLUM: Actinobacteria

### DESCRIPTION:

*Bifidobacterium adolescentis* is an anaerobic species of bacteria found in the gastrointestinal tracts of humans. It is one of the most abundant and prevalent *Bifidobacterium* species commonly found in adults. It contributes to the production of GABA, a neurotransmitter that plays a role in reducing stress and anxiety. Some strains can synthesise B vitamins, such as folic acid. *B. adolescentis* enhances the growth of all bifidobacteria.

### TREATMENT SUGGESTIONS:

Consider a probiotic supplement containing *B. adolescentis* and consuming prebiotic-rich foods like garlic, onions, and whole grains. Increase dietary fibre from fruits, vegetables, and legumes, and incorporate fermented foods such as yogurt and kefir.

**BIFIDOBACTERIUM BIFIDUM LOW:**

PHYLUM: Actinobacteria

### DESCRIPTION:

*Bifidobacterium bifidum* is a Gram-positive, anaerobic bacterium integral to the human gut microbiota, especially in infants. It ferments a variety of carbohydrates, including human milk oligosaccharides, aiding in digestion, and promoting a healthy gut flora. *B. bifidum* produces short-chain fatty acids that lower gut pH and inhibit pathogenic bacteria while supporting intestinal cells. It also modulates the immune system, enhancing immune responses and reducing inflammation, and strengthens the intestinal barrier. Clinically, *B. bifidum* has shown promise in alleviating gastrointestinal disorders.

**BIFIDOBACTERIUM BREVE LOW:**

PHYLUM: Actinobacteria

### DESCRIPTION:

*Bifidobacterium breve* is a Gram-positive, anaerobic bacterium that is commonly found in the human gastrointestinal tract, particularly in the intestines of infants. *B. breve* is known for its ability to metabolise various carbohydrates, including human milk oligosaccharides, which is essential for the development of a healthy gut flora in newborns. Studies demonstrate that *B. breve* exhibits several beneficial properties, including the production of short-chain fatty acids (SCFAs) such as acetate, which contribute to gut health by lowering pH and inhibiting the growth of pathogenic bacteria. Additionally, *B. breve* may alleviate symptoms of irritable bowel syndrome (IBS) and improve symptoms of atopic dermatitis.

**ESCHERICHIA SPECIES ELEVATED:**

PHYLUM: Proteobacteria

### DESCRIPTION:

*Escherichia* is a genus of Gram-negative, non-spore-forming, facultatively anaerobic, rod-shaped bacteria and normal inhabitants of the gastrointestinal tract. Species include *E. albertii*, *E. fergusonii*, *E. hermannii*, *E. marmotae* and most notably *E. coli*. High levels may be indicative of increased intestinal inflammatory activity and be associated with irritable bowel syndrome, Crohn's, ulcerative colitis and diarrhea. Studies have also revealed that chronic psychological stress may be associated with an increase in *E. coli* colonisation.



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**TREATMENT SUGGESTIONS:** Commensal probiotic cocktails are suggested to prevent and reverse gut elevated colonization.

**LACTOBACILLUS ACIDOPHILUS LOW:**

**PHYLUM:** Firmicutes

**DESCRIPTION:**

Lactobacillus acidophilus is a Gram-positive, rod-shaped, non-spore-forming bacterium commonly found in the human gut and fermented foods. It plays a key role in oxalate degradation, bowel normalisation and may assist patients with bloating.

**TREATMENT SUGGESTIONS:**

Consider probiotic supplementation containing L. acidophilus.

**LACTOBACILLUS CASEI LOW:**

**PHYLUM:** Firmicutes

**DESCRIPTION:**

Lactobacillus casei is a Gram-positive, rod-shaped, non-spore-forming, anaerobic probiotic bacterium involved in the fermentation of foods like cheese and yogurt. It produces antimicrobial substances, enhances gut barrier function, reduces pathogenic bacteria, and modulates the immune system. This bacterium is used to prevent and may assist various forms of diarrhea, including infectious diarrhea, traveller's diarrhea, and antibiotic-associated diarrhea.

**TREATMENT SUGGESTIONS:**

Consider probiotic supplementation containing L. casei and consuming fermented foods such as cheese and yogurt.

**LACTOBACILLUS DELBRUECKII LOW:**

**PHYLUM:** Firmicutes

**DESCRIPTION:**

Lactobacillus delbrueckii is a beneficial Gram-positive bacterium commonly found in the gut microbiome and known for its role in maintaining gastrointestinal health. It produces lactic acid through the fermentation of carbohydrates, contributing to a lower gut pH, which inhibits the growth of pathogenic microorganisms such as Clostridium and Candida species. Additionally, L. delbrueckii can enhance the intestinal barrier function and modulate the host immune response by promoting the production of anti-inflammatory cytokines. Its presence in the gut is associated with improved digestion and nutrient absorption, making it an important component in supporting overall gut health and microbial balance.

**LACTOBACILLUS PLANTARUM LOW:**

**PHYLUM:** Firmicutes

**DESCRIPTION:**

Lactobacillus plantarum is a Gram-positive, non-spore-forming, rod-shaped bacterium. L. plantarum plays a crucial role in gut health by enhancing intestinal barrier function, modulating the immune system, and inhibiting pathogenic bacteria. Additionally, it is beneficial for conditions such as irritable bowel syndrome, ulcerative colitis, and high cholesterol.

**TREATMENT SUGGESTIONS:**

Consider probiotic supplementation containing L. plantarum.

**LACTOBACILLUS RHAMNOSUS LOW:**

**PHYLUM:** Firmicutes

**DESCRIPTION:**

Lactobacillus Rhamnosus is a Gram-positive anaerobic bacterium and is one of the most widely used probiotic strains, of which various health effects are well documented including the prevention and treatment of gastro-intestinal infections and diarrhea and even preventing certain allergic symptoms.

Decreased Lactobacillus rhamnosus colonisation has been shown to decrease gastro-intestinal health, increasing the risk of gastro-intestinal infections and diarrhea as well as extra-intestinal infections including oral and respiratory health. Studies have also revealed that chronic psychological stress and alcohol use may be associated with a decrease in Lactobacillus species, as well as antibiotic / medication use.

**TREATMENT SUGGESTIONS:** Treatment may involve the use of Lactobacillus containing probiotics and treatment of any intestinal



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**-.SHIREE WALKER**  
**GLOW AESTHETICS PERTH**  
**54B ANGOVE STREET**  
**NORTH PERTH WA 6006**

**KRYSTIELEE HARRISON**  
**10-Sep-1987**      **Female**

**11 FREEMAN VIEW**  
**BUSHMEAD WA 6055**

**LAB ID :** 4115353  
**UR NO. :** 6662742  
**Collection Date :** 23-Jun-2025  
**Received Date:** 25-Jun-2025



**4115353**

infections.

**LACTOBACILLUS SALIVARIUS LOW:**

**PHYLUM:** Firmicutes

**DESCRIPTION:**

Lactobacillus salivarius is a Gram-positive, rod-shaped, non-spore-forming bacterium predominantly found in the human oral cavity, gastrointestinal tract, and vagina. It plays a significant role in maintaining oral and gut health by producing lactic acid and bacteriocins, which inhibit the growth of pathogenic bacteria. L. salivarius enhances gut barrier function, modulates the immune system, and helps in the digestion of proteins and complex carbohydrates. It has been studied for its potential benefits in managing conditions such as irritable bowel syndrome (IBS), periodontal disease, and atopic dermatitis, highlighting its importance in promoting overall health and preventing infections.

**TREATMENT SUGGESTIONS:**

Consider L. salivarius as a probiotic strain which may improve intestinal permeability and immune response.

**OXOLOBACTER FORMIGENES LOW:**

**PHYLUM:** Proteobacterium

**DESCRIPTION:**

Oxalobacter formigenes is a Gram negative oxalate-degrading anaerobic bacterium. Oxalate is formed in the liver by amino acid catabolism as well as present in a wide range of foods including tea, coffee, chocolate and certain fruits and vegetables. High concentration of oxalate in the urine is related to the potential formation of calcium oxalate kidney stones. Oxalobacter Formigenes is the main known bacterial species involved in oxalate degradation in the gut and maintains oxalate homeostasis. Levels of O. Formigenes tends to decrease with age as well as with the use of antibiotics or other drugs. Low levels may be associated with calcium oxide stone formation, inflammatory bowel disease or Crohn's.

**TREATMENT SUGGESTIONS:**

Treatment options include probiotic treatment and low oxalate diet modification. Urinary oxalate levels may also need to be investigated.



# The Four “R” Treatment Protocol

REMOVE	Using a course of antimicrobial, antibacterial, antiviral or anti parasitic therapies in cases where organisms are present. It may also be necessary to remove offending foods, gluten, or medication that may be acting as antagonists.  Consider testing IgG96 foods as a tool for removing offending foods.	ANTIMICROBIAL	Oil of oregano, berberine, caprylic acid
		ANTIBACTERIAL	Liquorice, zinc carnosine, mastic gum, tribulus, berberine, black walnut, caprylic acid, oil of oregano
		ANTIFUNGAL	Oil of oregano, caprylic acid, berberine, black walnut
		ANTIPARASITIC	Artemesia, black walnut, berberine, oil of oregano
		ANTIVIRAL	Cat's claw, berberine, echinacea, vitamin C, vitamin D3, zinc, reishi mushrooms
		BIOFILM	Oil of oregano, protease
REPLACE	In cases of maldigestion or malabsorption, it may be necessary to restore proper digestion by supplementing with digestive enzymes.	DIGESTIVE SUPPORT	Betaine hydrochloride, tilactase, amylase, lipase, protease, apple cider vinegar, herbal bitters
REINOCULATE	Recolonisation with healthy, beneficial bacteria. Supplementation with probiotics, along with the use of prebiotics helps re-establish the proper microbial balance.	PREBIOTICS	Slippery elm, pectin, larch arabinogalactans
		PROBIOTICS	Bifidobacterium animalis subsp. lactis, lactobacillus acidophilus, lactobacillus plantarum, lactobacillus casei, bifidobacterium breve, bifidobacterium bifidum, bifidobacterium longum, lactobacillus salivarius, lactobacillus paracasei, lactobacillus rhamnosus, Saccaromyces boulardii
REPAIR & REBALANCE	Restore the integrity of the gut mucosa by giving support to healthy mucosal cells, as well as immune support. Address whole body health and lifestyle factors so as to prevent future GI dysfunction.	INTESTINAL MUCOSA IMMUNE SUPPORT	Saccaromyces boulardii, lauric acid
		INTESTINAL BARRIER REPAIR	L-Glutamine, aloe vera, liquorice, marshmallow root, okra, quercetin, slippery elm, zinc carnosine, Saccaromyces boulardii, omega 3 essential fatty acids, B vitamins
		SUPPORT CONSIDERATION	Sleep, diet, exercise, and stress management